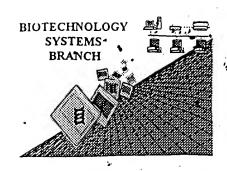
### RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/7019268
Source:	PCT 09 BEST AVAILABLE COPY
Date Processed by STIC:	11/14/01 BEST AVAILABLE COPT

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 c-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 c-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

#### Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

### Raw Sequence Listing Error Summary

ERROR DETECTED	SUCCESTED CORRECTION SERIAL NUMBER: 09/201926 A
ATTN: NEW RULES CAS	ES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY
1Wrapped Nucleics Wrapped Aminos	The numberNext at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
JMisslighed Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length.	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6Patentin 2.0 "bug"	A "bug" in Patentin version 2.0 has equiped the <220>-<223> section to be missing from a mino acid sequences(s). Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
· · · · · · · · · · · · · · · · · · ·	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.
8Skipped Sequences' (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence 10 pequence id number <400> sequence id number
n 1 /	000
9 Use of n's or Xxx's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valld <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is regulred when <213> response is Unknown is Artificial Sequence
Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
Misuse of n	in tan only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

PCT09

```
DATE: 11/14/2001
                      RAW SEQUENCE LISTING
                      PATENT APPLICATION: US/09/701,926A
                                                                  TIME: 13:53:41
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                      Output Set: N:\CRF3\11142001\I701926A.raw
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      5 <120> TITLE OF INVENTION: PHENOTYPE MODIFYING GENETIC SEQUENCES
      7 <130> FILE REFERENCE: 111590-120
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     13 <151> PRIOR FILING DATE: 1998-06-04
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     15 <150> PRIOR APPLICATION NUMBER: PP6174
     16 <151> PRIOR FILING DATE: 1988-09-25
                                                                   See pager 2, 4 and 8
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     21 <150> PRIOR APPLICATION NUMBER: PP3903
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Corrected Diskette Needed
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Field 222 (1.0.6263)
Field 222
ERRORED SEQUENCES
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     87 <400> SEQUENCE: 3
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A

Input Set : A:\sequencelisting.txt

Output Set: N:\CRF3\11142001\1701926A.raw

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     116 aataqttcaq acaaqttaat qaccaactta tatattaqtt caatccataa aatttqatgt 1740
     117 agtagttaca aaatggaatt gcttgaaggc ttatgccatg ttttatgcca ggttatatgc 1800
     118 caggaaggtt gtatgactag gatgcttcca agtttggaaa tcagcaacaa ctgaaaactc 1860
     119 ttattaaggc tttaacatga ccacgggatc aaatcggttg ctgatatagt gataaatcat 1920
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E--> 137 aagthggatg tttacttggc agctgaggcc gaggccatgt ttgantgtta tgcttatagg 3000
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     158 taactactca gatgctaaaa cgacgccgtc ttccactgat cggaaacaga gcaaaacccc 4260
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> whowever

Input Set : A:\sequencelisting.txt

Output Set: N:\CRF3\11142001\1701926A.raw

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     202 accettaaat gtagggaatt tgaagtttta aaaaccacac tttgttattt attggcccaa 180
    203 atactcgata atctttacat tattgaaaat caacattcaa aaggaacgaa ccttcaatca 240
    204 caccatcaat gtcaactttc ttttattttg gataatctaa gtttttaaat tgcagtaaaa 300
E--> 205 tnaaataaaa ccctaaactt cttctaggtt gagacttagt aaatatgaat tatataaaga 360
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    209 taattacaaa toottaaata gataaaagot acgaataaca taatatoott aaatagataa 600
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E--> 210 aagctacgaa taacataata gtatattact ccnaattatt ttgatttatt taaaatgact 660

Input Set : A:\sequencelisting.txt

Output Set: N:\CRF3\11142001\I701926A.raw

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     270 <211> LENGTH: 886
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     275 ccqctcatqa tccctqaaaq cqacqttqqa tqttaacatc tacaaattqc cttttcttat 60
     276 cgaccatgta cgtaagcgct tacgtttttg gtggaccctt gaggaaactg gtagctgttg 120
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     278 gcaccggtga gtaatattgt acggctaaga gcgaatttgg cctgtagacc tcaattgcga 240
     279 qctttttaat ttcaaactat tcgggcctaa cttttggtgt gatgatgctg actggacaaa 300
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     287 ttgcactatt tgcaattata gagcttaaat atagccagtg ttttctgact aaacgaacga 780
     288 ttgagatcaa aaatacaatt ccacatatag cacctgaaat aagtaacgga cctgagaaca 840
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     311 qaatcaacaa aaagcaagta gaatgtatca ctcacattaa cttgcacaaa gaaattcttt 180
     312 ggctcataac aactgctgat cttgaaaaag gaagaaaaac agatatttac aaagagagac 240
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     317 aacgattgag atcaaaaata caattccaca tatagcacct gaaataagta acggacctga 540
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     320 <210> SEQ ID NO: 12
                                                    The type of errors shown exist throughout
     321 <211> LENGTH: 1619
                                                    the Sequence Listing Page check subsequent
     322 <212> TYPE: DNA
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                                                    sequences for similar errors.
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     327 aaatgettet tteatgtaea teeagtgetg tetgeaaget teattaatet taetettaet 120
     328 caacaatttt cacttttctt caggaggatt ttaacgtgtg gaatttctgg agacttccac 180
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     331 gtgatgctga aattatagga attcgttaca tcagtgtaga ttccgaacac agtctgtgtg 360
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The type of errors shown exist throughout the Sequence Listing. Please cheek subsequent seduences for similar errors.

Input Set : A:\sequencelisting.txt

Output Set: N:\CRF3\11142001\1701926A.raw

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334 tggctagtgt atatagtatt gtcttatatc cgtcatcttg gaggaagaaa atcgtgtcct 540
     335 cagttttctg atattctgct catcaatcat cgactagcca atacactttg gccctacata 600
     336 tacacatact tatgagaagg aaaatacgaa atacgctcct tcaagacgag ttgaactttg 660
     337 taaattgttg tagtattagt atatgttaat gaggaaatgt agattttgtt gtagtttggt 720
     338 gatttgtaga atctgtctta taaagggact tacatgttga ggcaaactgt ataaaggtta 780
     339 aattgtcaat aacacacatc aaaatattgg accagtattt taagtaattt tttctgtata 840
     340 aaggetatgt tgeteaaate etteaaaaat etegacagat geatggeace ggtagtgeat 900
     341 ttttttgaat gagctggata cgagtgcaat aatatatttg ggaagtttga gcaaaataga 960
     342 cctqaaatta cttttagctt ttcttttta aaggaatcgg atatgggtac aataatattt 1020
     343 ttgaagagtc tgagcaacat agactactct cggtaggatg aggataagat tgaaatttta 1080
E--> 344 aaatgctcta aagagaaaat ttgtggataa gattctccac taatttttnt atgacatgat 1140
     345 gagattetge ctaagagtte caagaatatg gtgcacetgt taataatgta tatattataa 1200
     346 tagcataatc cactgttatg attttagcaa gctccttttt gtaatatatg aatgaacata 1260
     347 aatataaaaa aggagagtta tatttgaacc atataaaaaa tgttacaagt atttttatat 1320
     348 gaataatata ataaaaagta aaccttttcg acaaaaaatt gattcatttc cctttttaac 1380
     349 aattataacg gtttttaaat cctaatatac acctagtaaa aatatctatt tcaacccttc 1440
     350 tegeagetgt attgeetaaa acceatatea eecceaegta geetaaaatt taetttatae 1500
     351 tacqttqttt tqtttctcat ttttatttat ctttaattta tatcctqtaa aaagactcaa 1560
     352 agatgttttc tttaaatttt actitatttt ttttaggata aaaaatttgc aattcctaa 1619
     354 <210> SEQ ID NO: 13
                                          Field 222 (120 ... 1193)
     355 <211> LENGTH: 1193
     356 <212> TYPE: DNA
     357 <213> ORGANISM: Tomato
     359 <400> SEQUENCE: 13
     360 tgagtagaag ataaacttga caacgcatta gctcgaataa gagcataaat aaaaaagttt 60
     361 taactttaag aatccqtqca aaaaatcatc tactcaatta actcqatcaa tattctttca 120
     362 teggtaactt acceptttgg tattatatgt gtaaatatac etaaatataa atacgagtet 180
     363 ataataacct aataaaaata ttaggcataa tagcggtgtt gttttgttag actcagtatt 240
     364 ttttatattt tataaaataa atactacgct ctttcaccaa acaattcttc aacgttaaat 300
     365 attettgacg gttttgttet gaaactatga ttetetttta gattttggtt ttgttgattt 360
     366 ctgatcaaaa actaaaagag aataattett eteecatttt attgetatet ttttatgatt 420
     367 gatttgttgg gggttcagca aatttattta tgttctttta gtttttcctc ttttatctgt 480
     368 atttgaatct tgatcaatta atgttctttg atcatttgtt tgttagaatc caaatacgcg 540
     369 agcaagagaa aaagatttag gaaatgagta aagattggat ttttatggga aagatctaaa 600
     370 gatttggttg aagggattaa tgaattgagc atatgagcta aaaaatcaat cttggtgagt 660
     371 agggtatgtt atttgtggaa gttttgttag cttttcttgt atgtattgat attagatgat 720
E--> 372 ttaaacagag tcactaacat tcatatagct gaccttgaat tgtttaggnc agtggcgtag 780 5
     373 tagttgttgt tgttataaga gaatgagtgc tatggggagg ataggtagtt acataggtag 840
E--> 374 aggggtacgt agtgtttcgg ggacgttgaa tccatttggt ggtnctgtgg atatcattgt 900
     375 ggtgaggcag ccagatggga gtttgaaatc aactccttgg tatgttagat ttgggaagat 960
     376 tcagggggtt ttgaaggcta gagaaaatgc ggttaatgta agtgtcaatg gcgttgaagc 1020
     377 tggttttcgt atgaatttag atactagagg gcaggcatac ttcctaaggg agcgagacat 1080
     378 ggaaaatgga tattetttaa etaetegaae atttgaacaa ettgeaeett tgaatetgaa 1140
E--> 379 ggaggaaaga atgtggttga ttcncctgct caaaacccca gcccgggccg tcg
                                                                           1193
     381 <210> SEQ ID NO: 14
     382 <211> LENGTH: 222
     383 <212> TYPE: DNA
     384 <213> ORGANISM: Tomato
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386 <400> SEOUENCE: 14

Input Set : A:\sequencelisting.txt

Output Set: N:\CRF3\11142001\I701926A.raw

E--> 387 tatgttgctc aaatccttca aaaatctcga cagatgcatg nnnnnnnnn cacccggtag 60 388 tgcatttttt tgaatgagct ggatacgagt gcaataatat atttgggaag tttgagcaaa 120 E--> 389 atagacctga aattactttt agcttttctt ttttaaagnn nnnnnnnnn nngaatcgga 180 E--> 390 tatgggtaca ataatatttt tgaagagtcn tgagcaacat ag 392 <210> SEQ ID NO: 15 393 <211> LENGTH: 222 394 <212> TYPE: DNA 395 <213> ORGANISM: Potato 397 <400> SEOUENCE: 15 398 tatgttgctc aaacacttca aaaatgtcca caggtgcgtg tcggatactc caaaaagtag 60 E--> 399 tqtatttaqq tqtqtqnnnn tqatattaqt nnnaqtqtat atttaqqntq tqtqtqqata 120 E--> 400 gtagnnntgt atttagatgt gtgtgatatt tcaaaaagtt gtgtattttg gagaatttga 180 401 tacqqqtqcq gcaacaattt tqaaqaqtca qgaqcaaaat ag 222 531 <210> SEQ ID NO: 32 532 <211> LENGTH: 1588 533 <212> TYPE: DNA 534 <213> ORGANISM: Tomato 536 <400> SEQUENCE: 32 537 atcaagttga aatatgttaa caaaatgtac agttttatta tttttatttt atttataaaa 60 538 aaaaaattgt acaaagaaac aaaatccctt ccttctgtat ttccatgtga tgtttaaatg 120 539 gcatttgagt aaaagccaca aaaggcccat gtgaaattta taaaattttg aaacattttt 180 540 gcataacaaa acaatacata agaggacacg taaaaacttac taaaagagtt tttagttacg 240 541 tataagcaaa gtttgagatt cccaagaaga aagagtttga aaatactaaa tgtcttgttg 300 542 tcatccatat atatatatat gaatgaattc tcacatttgt gatcaagatt tctttatgca 360 E--> 543 tgntaatatt tatatttgga aattaaccgt cgattaatta agattatcat tgaataaggt 420 544 ttgaaaaaga taaattgaac tatttcactt ttggagtgtt attgttatct gctaggtcaa 480 546 tgaggttgta ctaaaggaca tataaaaagg tgaaaaagct aaaagtttca ctaataacta 600 547 attittatit tactitigtet tgtgtactaa actittecat gtetitteet ticaattiee 660 548 agttgtgatg gatagtaaat tttctatagc attcaacaca aggacaaaac actaagcaac 720 549 aaaagcatcc aaaaaccaag attagcaatg tgcaaatgaa gctttatgta tgatcaaaaa 780 550 cacaacttgg aagttggaac tacctatctt agattccatc acttttttt tgttctccat 840 551 cgatattcat cgatattcag tattcgagct ccgattaaat cataattcga taaagcgtac 900 552 tttaataaaa ataatttcac tcgaaggett caatctgaaa ccactgatta ttaaaaatga 960 553 aagaatteta teattattee atatettttt aggagattea agttaaaata gacaacettt 1020 554 ttetttaaat attgteacaa tggtaataga tgeatgegeg eetaatttea eattttttaa 1080 555 tataccagge tateattaae tttttttta tttaaaaaae tttaatgatt tegaagaaat 1140 556 aatgactata taaaaaaaac aagaaatatt agtagccatc attatgtata tgagcaaaca 1200 557 aaacgaaaat ggaactatgg caacatcatg gaagctagga ataaacagct ccacttcaca 1260 558 agagaacaaa gttcatgttg tactattata ccttttttta ttttgacctc ttttaatatc 1320 559 gtatatatta agcaagttgt taatcatata ccatctttta aatatttact tttgaaatca 1380 560 taaaaaaatt gatgaaaaaa gttattatca tatctgttct tgcgtgagaa ataacaaata 1440 561 tatttaagat gcacaaaaat tgattcgaac tagacttttt ttaaaaaaaaa ataaaaaaca 1500 562 tgatgaaact ctaggtgggg tattcttttt gtcaattact actaacaaag attgttgaaa 1560 563 aagaagccaa ttatatgatt catcaata 565 <210> SEQ ID NO: 33 566 <211> LENGTH: 1307 567 <212> TYPE: DNA 568 <213> ORGANISM: Tomato

Input Set : A:\sequencelisting.txt

Output Set: N:\CRF3\11142001\1701926A.raw

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570 <400> SEQUENCE: 33
     571 ttggacttcc tacccagcag ttcacacatc aatatcattt aattaaaatt aaagccattt 60
     572 atttaggaaa taaatagcat aaaaaaaaca ctaataatta aaacatttgt gtcaaaggga 120
     573 aagtatattg actaattttt tgcatatgtg gttcaaagga ggaatttttt aattacaaaa 180
     574 aaaaaagttt tatggtggga atcaaacata ttataggata attaaagaga tggatttatt 240
     575 atattttgtg taatctatta attattaaat ggcttaattt tgtatccact aataatataa 300
     576 qtaatttcta tatattcagt acaatttgac taqctccaac agctttccca gtaacacata 360
     577 tttatacagt tgcatctcac tataataaaa atatgtaaat attttctctt taccgtaact 420
     578 ccagtaaaac ttaaactcta attaataata caacactaat ctaggcaagc tgtagactgt 480
     579 aattaattgc atgttttaaa tctgtgaagg gtcgtttggc ataaaaatac ataatgcagg 540
     580 gattattaac gtatagatta gtaatacata gattagtaat gcatggatta gtttttatca 600
     581 agtgtttgat tcattgtttc ctacttaatc ttatgtttag tttaaaactc tagaaaaata 660
     582 tatttcctat tatacctttg agttattgtg agaatttgta tttcatttaa ctagtcaagt 720
E--> 583 taaatncnaa tttatatata tatatatata ttattaattt tgaggtgtga tatgtcacac 780
     584 tgtatatttt taattttttg ttggtcaaat ataccttgaa cttaaacatg gatttaaggc 840
E--> 585 tatttaaatt gttcaaatac acgaacctta tttttttat aaaanaatca agtggtcaat 900
E--> 586 cgcaaactac atttataaaa naaaggccaa aaaaatcaat ccaatataac agctcataca 960
     587 tggagaaaaa attagtttat gaaatcatca aattacatgg aataaatttg gagaatttaa 1020
E--> 588 atgaatattt ataaatattt tcatataaat aaaaaagaac attaattaca aatanaataa 1080
     589 tagaaaaaa atttgaggat attttagtca ttttggaatc ttttcgaagg attgctaaac 1140
     590 cttqaattaq ctatccctcc atttcctagg gataaaataa gaccttgtat gaggtataac 1200
     591 taatctatgg attaggttaa ataaagtaac caaacaatat ttttgttgga ctaaatttta 1260
E--> 592 atccatggat tenttggatt aataceteet accageeegg geegteg
     594 <210> SEQ ID NO: 34
     595 <211> LENGTH: 255
     596 <212> TYPE: DNA
     597 <213> ORGANISM: Tomato
     599 <400> SEQUENCE: 34
     600 ggtcgtttgg cataaaaata cataatgcag ggattattaa cgtatagatt agtaatacat 60
     601 agattagtaa tgcatggatt agtttttatc aagtgtttga ttcattgttt cctacttaat 120
E--> 602 cttatgttta gtttaaaact ctagaaaaat anntatttcc tattatacct ttgagttatt 180
E--> 603 gtgagaattt gtatttcatt taactnagtc aagttaaatn cnaatttata tatatatata 240
     604 tatattatta atttt
                                                                            255
     606 <210> SEQ ID NO: 35
     607 <211> LENGTH: 255
     608 <212> TYPE: DNA
     609 <213> ORGANISM: Tomato
     611 <400> SEQUENCE: 35
E--> 612 gatcgtacgg tacaaagatc aatacttcag gnnnnnnnn nnnnnngagt agtaatacat 60
E--> 613 tttttggtaa tgcagagatt antttttatc aagtgtttgg ttcattgttt nttacctaat 120
     614 tttgtgtgtg gtttaaagtt tacaaaaaat aattetttee aattataege taaagttatt 180
E--> 615 atgagatttt atatttcatg taattgggtc aannnaatag ataattgacc gataatatta 240
     616 ttttttataa cattt
     647 <210> SEQ ID NO: 39
     648 <211> LENGTH: 197
     649 <212> TYPE: DNA
     650 <213> ORGANISM: Tomato
     652 <400> SEQUENCE: 39
E--> 653 ttatatattt gtatttgtat aaagtgaaag agacgatgnn gagagtagcg agcgagatta 60
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,926A

DATE: 11/14/2001 TIME: 13:53:41

Input Set : A:\sequencelisting.txt

Output Set: N:\CRF3\11142001\1701926A.raw

E--> 654 aaaaagagtg gcgaacgnnn nnagatatgc cgtaaattag aattaaatga aactgtcatt 120

E--> 655 ataacattta ttttgaataa ataattttga tataatacac aattttcnnt taaaaagcaa 180

E--> 656 cgannnnnng ataatgt

- 1

E--> 659

# VERIFICATION SUMMARY PATENT APPLICATION: US/09/701,926A DATE: 11/14/2001 TIME: 13:53:42

Input Set : A:\sequencelisting.txt
Output Set: N:\CRF3\11142001\I701926A.raw

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:136 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
M:340 Repeated in SeqNo=3
L:200 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:285 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:314 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:326 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
M:340 Repeated in SeqNo=12
L:372 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:387 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
M:340 Repeated in SeqNo=14
L:399 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:543 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:583 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
M:340 Repeated in SeqNo=33
L:602 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
M:340 Repeated in SeqNo=34
L:612 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
M:340 Repeated in SeqNo=35
L:653 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
M:340 Repeated in SeqNo=39
L:659 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:197 SEQ:39
```